



results of BLAST

BLASTN 2.2.15 [Oct-15-2006]

RID: 1167425726-9360-210999924966.BLASTQ1

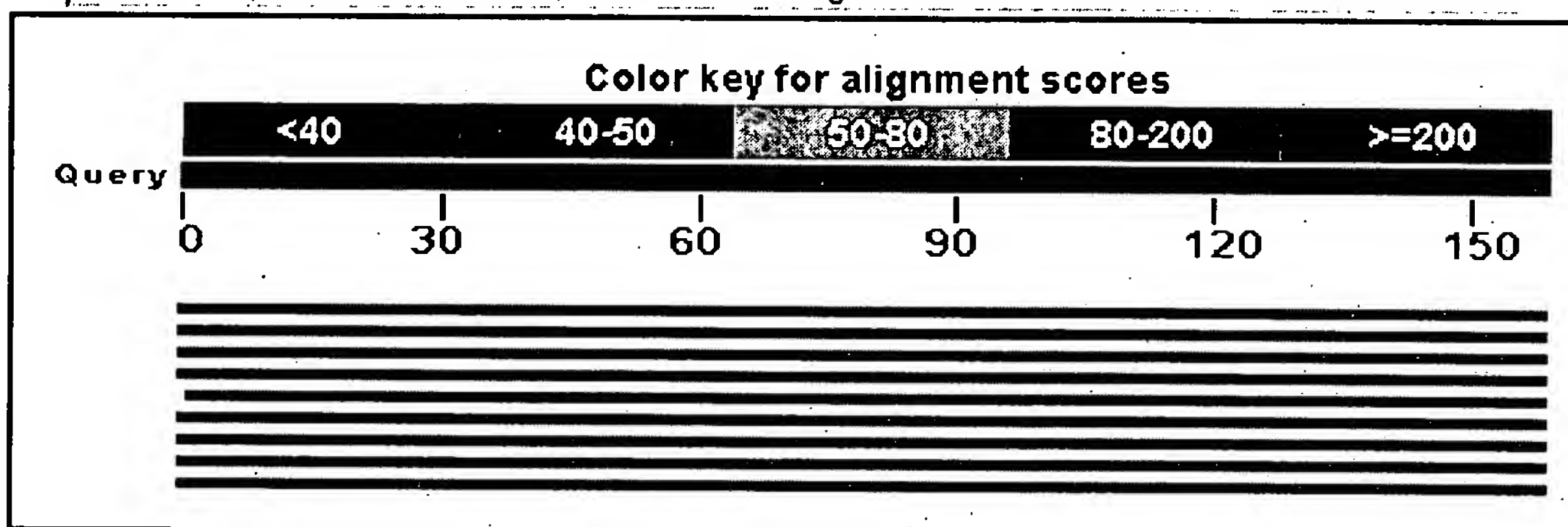
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
4,720,951 sequences; 18,839,166,270 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=158

Distribution of 9 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



[Distance tree of results](#) NEW

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** M

Sequences producing significant alignments:
(Click headers to sort columns)

Accession	Description	Max score	Tot score	Query coverage	v
AY119786.1	Karenia brevis ribulose-1,5-bisphosphate carboxylase/oxygenase	292	292	100%	2
AY251790.1	Karenia brevis ribulose-1,5-bisphosphate carboxylase/oxygenase	287	287	100%	8
AY154881.1	Karenia brevis strain Charlotte Harbor C2 ribulose-1,5-bisphosphate	287	287	100%	8
AY154879.1	Karenia brevis strain Mexico Beach C5 ribulose-1,5-bisphosphate	287	287	100%	8
AY154878.1	Karenia brevis strain Charlotte Harbor A2 ribulose-1,5-bisphosphate	285	285	99%	3
AY154882.1	Karenia brevis strain Piney Island A9 ribulose-1,5-bisphosphate	281	281	100%	4

	gene for plastid product				
AY154880.1	Karenia brevis strain Piney Island B4 ribulose-1,5-bisphosphate	281	281	100%	4
AY154883.1	Karenia brevis strain Mexico Beach B3 ribulose-1,5-bisphosphate	276	276	100%	2
AY154877.1	Karenia brevis strain Appalachicola C6 ribulose-1,5-bisphosphate	276	276	100%	2

Alignments

Get selected sequences	Select all	Deselect all	Distance tree of results
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> ☐ gb|AY119786.1| Karenia brevis ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcL) gene, partial cds; chloroplast gene for chloroplast product
Length=907

Score = 292 bits (158), Expect = 2e-76
Identities = 158/158 (100%), Gaps = 0/158 (0%)
Strand=Plus/Plus

```

Query 1      GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60
             |||
Sbjct 298    GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 357

Query 61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120
             |||
Sbjct 358    ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 417

Query 121    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
             |||
Sbjct 418    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 455
    
```

> ☐ gb|AY251790.1| Karenia brevis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) mRNA, partial cds; chloroplast gene for chloroplast product
Length=553

Score = 287 bits (155), Expect = 8e-75
Identities = 157/158 (99%), Gaps = 0/158 (0%)
Strand=Plus/Plus

```

Query 1      GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60
             |||
Sbjct 1      GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60

Query 61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120
             |||
Sbjct 61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120

Query 121    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
             |||
Sbjct 121    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
    
```

> ☐ gb|AY154881.1| Karenia brevis strain Charlotte Harbor C2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial

cds; plastid gene for plastid product
Length=553

Score = 287 bits (155), Expect = 8e-75
Identities = 157/158 (99%), Gaps = 0/158 (0%)
Strand=Plus/Plus

```
Query 1      GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60
             |||
Sbjct 1      GATGATGAAAATATTAACTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60

Query 61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120
             |||
Sbjct 61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120

Query 121    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
             |||
Sbjct 121    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
```

> [gb|AY154879.1](#) Karenia brevis strain Mexico Beach C5 ribulose-1,5-bisphosphate
carboxylase/oxygenase large subunit (rbcL) gene, partial
cds; plastid gene for plastid product
Length=553

Score = 287 bits (155), Expect = 8e-75
Identities = 157/158 (99%), Gaps = 0/158 (0%)
Strand=Plus/Plus

```
Query 1      GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60
             |||
Sbjct 1      GATGATGAAAATATTAACTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60

Query 61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120
             |||
Sbjct 61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120

Query 121    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
             |||
Sbjct 121    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
```

> [gb|AY154878.1](#) Karenia brevis strain Charlotte Harbor A2 ribulose-1,5-bisphosphate
carboxylase/oxygenase large subunit (rbcL) gene, partial
cds; plastid gene for plastid product
Length=553

Score = 285 bits (154), Expect = 3e-74
Identities = 156/157 (99%), Gaps = 0/157 (0%)
Strand=Plus/Plus

```
Query 2      ATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCTA 61
             |||
Sbjct 2      ATGATGAAAATATTAACTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCTA 61

Query 62     TGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAATG 121
             |||
Sbjct 62     TGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAATG 121
```

```
Query 122 TCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
          |||
Sbjct 122 TCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
```

> [gb|AY154882.1|](#) *Karenia brevis* strain Piney Island A9 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gene for plastid product
Length=553

Score = 281 bits (152), Expect = 4e-73
Identities = 156/158 (98%), Gaps = 0/158 (0%)
Strand=Plus/Plus

```
Query 1 GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60
          |||
Sbjct 1 GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60

Query 61 ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120
          |||
Sbjct 61 ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120

Query 121 GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
          |||
Sbjct 121 GTCACGACAGCGACGATGGAAGACATGTATGAAAGAGC 158
```

> [gb|AY154880.1|](#) *Karenia brevis* strain Piney Island B4 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gene for plastid product
Length=553

Score = 281 bits (152), Expect = 4e-73
Identities = 156/158 (98%), Gaps = 0/158 (0%)
Strand=Plus/Plus

```
Query 1 GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60
          |||
Sbjct 1 GATGATGAGAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60

Query 61 ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120
          |||
Sbjct 61 ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120

Query 121 GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
          |||
Sbjct 121 GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
```

> [gb|AY154883.1|](#) *Karenia brevis* strain Mexico Beach B3 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gene for plastid product
Length=553

Score = 276 bits (149), Expect = 2e-71
Identities = 155/158 (98%), Gaps = 0/158 (0%)
Strand=Plus/Plus

```
Query 1 GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60
```

12/29/2006

Length of database: 18839166270
Length adjustment: 30
Effective length of query: 128
Effective length of database: 18697537740
Effective search space: 2393284830720
Effective search space used: 2393284830720

A: 0

X1: 13 (25.0 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 13 (25.1 bits)

S2: 20 (38.1 bits)

**results of BLAST****BLASTN 2.2.15 [Oct-15-2006]**

RID: 1167424902-29846-208565337440.BLASTQ1

Database: GenBank non-mouse and non-human EST entries
27,698,245 sequences; 15,888,380,909 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

Query=
Length=158

No significant similarity found. For reasons why, [click here](#).

Database: GenBank non-mouse and non-human EST entries

Posted date: Dec 27, 2006 6:00 PM

Number of letters in database: -1,291,488,271

Number of sequences in database: 27,698,245

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 27698245

Number of Hits to DB: 456698

Number of extensions: 0

Number of successful extensions: 0

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Length of query: 158

Length of database: 15888380909

Length adjustment: 30

Effective length of query: 128

Effective length of database: 15057433559

Effective search space: 1927351495552

Effective search space used: 1927351495552

A: 0

X1: 12 (23.1 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 12 (23.3 bits)

S2: 20 (38.1 bits)